

Delaval, Jan

123453

From: Gambel, Phillip
Sent: Monday, June 07, 2004 9:21 AM
To: Delaval, Jan
Subject: sequence search for 09/ 816,697

jan

please perform a sequence and a sequence interference search

09/ 816,697

SEQ ID NO: 2 (lorenz slic)

thanx

phillip gambel
at unit 1644
272-0844

1644 maiblox 3c70



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 123953

TO: Phillip Gambel
Location: 3e81 / 3c70
Monday, June 07, 2004
Art Unit: 1644
Phone: 272-0844
Serial Number: 09 / 816697

From: Jan Delaval
Location: Biotech-Chem Library
Rem 1A51
Phone: 272-2504

jan.delaval@uspto.gov

Search Notes

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Att Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg Room Location: _____ Results Format Preferred (enter: PAPER DISK E-MAIL): _____

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept of novelty in the invention. Define any terms that may have a special meaning. Give examples of relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher _____	NA Sequence (H) _____	STN _____
Searcher Phone #. 22504	AA Sequence (H) <input checked="" type="checkbox"/>	Dialog _____
Searcher Location _____	Structure (H) _____	Questel/Orbit _____
Date Searcher Picked Up 6/7	Bibliographic _____	Dr. Link _____
Date Completed: 6/7	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Technical Prep Time 60	Patent Family _____	WWW/Internet _____
Online Time 40	Other _____	Other (specify) _____

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2004, 09:29:08 ; Search time 18 Seconds

(without alignments)

314.120 Million cell updates/sec

Title: US-09-816-697A-2

Perfect score: 1650

Sequence: 1 MASPEHPGPGCMGPITQCT.....RRTPRGITLKELTVREYLH 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1253.5	76.0	313	1 SNXK_MOUSE	Q9d2y5 mus musculus
2	413.5	25.1	373	1 SNXK_HUMAN	Q969t3 homo sapien
3	123	7.5	342	1 SNXK_MOUSE	Q9nrs6 homo sapien
4	118	7.2	169	1 SNXO_HUMAN	Q9y343 homo sapien
5	112.5	6.8	435	1 SNXR_HUMAN	Q96192 homo sapien
6	111	6.7	2477	1 SPCK_CHICK	P07751 gallus gall
7	102.5	6.2	1127	1 MDML_YEAST	Q01846 saccharomyc
8	102	6.2	2472	1 SPCK_RAT	P16086 rattus norv
9	100.5	6.1	343	1 SNXG_HUMAN	P57768 homo sapien
10	99.5	6.0	1068	1 DAM2_MOUSE	Q80u19 mus musculus
11	99	6.0	2472	1 SPCK_HUMAN	Q13813 homo sapien
12	98.5	6.0	204	1 SNXN_HUMAN	Q96193 homo sapien
13	98.5	6.0	705	1 SYN1_HUMAN	P17600 homo sapien
14	97	5.9	2702	1 SNXB_HUMAN	Q9y5w9 homo sapien
15	97	5.9	595	1 SNX9_MOUSE	Q91vh2 mus musculus
16	97	5.9	4684	1 PLE1_HUMAN	P17600 homo sapien
17	96.5	5.8	387	1 SNX7_HUMAN	Q9unh6 homo sapien
18	96	5.8	595	1 SNX9_HUMAN	Q9y5x1 homo sapien
19	95.5	5.8	339	1 NCF4_MOUSE	P97369 mus musculus
20	95.5	5.8	387	1 SNX7_MOUSE	Q9cy18 mus musculus
21	95.5	5.8	580	1 SKR1_SCHPO	Q94547 schizosacch
22	95	5.8	943	1 UVRA_UREPA	Q9pr42 ureaplasma
23	94.5	5.7	496	1 SGK3_MOUSE	Q9ere3 mus musculus
24	93.5	5.7	496	1 SGK3_HUMAN	Q96br1 homo sapien
25	92.5	5.6	450	1 SNX4_HUMAN	Q95219 homo sapien
26	92	5.6	706	1 SYN1_BOVIN	P17599 bos taurus
27	92	5.6	3674	1 SPCR_HUMAN	Q9nrc6 homo sapien
28	91.5	5.5	327	1 PKB6_MOUSE	Q91xw8 mus musculus
29	91	5.5	1565	1 DMN_HUMAN	O15061 homo sapien
30	90.5	5.5	193	1 SNXK_HUMAN	O15061 homo sapien
31	90.5	5.5	344	1 SNXK_RAT	Q96194 homo sapien
32	90	5.5	1446	1 TE18_PRRVA	P57769 rattus norv
33	90	5.5	1461	1 IE18_PRRVF	P33479 pseudorabie
					P11675 pseudorabie

RESULT 1

SNXK_MOUSE

ID SNXK_MOUSE STANDARD; PRT; 313 AA.

AC Q9D2Y5;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Sorting nexin 20.

GN SNX20.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RA Hong W.;

RT *A new member (SNX20) of the sorting nexin protein family.*;

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cecum;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,

RA Nordone P., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,

RA Hayashizaki Y.;

RT *Functional annotation of a full-length mouse cDNA collection.*;

RL Nature 409:685-690(2001).

CC -!- FUNCTION: May be involved in several stages of intracellular

CC trafficking [by similarity].

CC -!- SIMILARITY: Belongs to the sorting nexin family.

CC -!- SIMILARITY: Contains 1 phox homology (PX) domain.

CC -----

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CC -----

ALIGNMENTS

```

DR EMBL; AF395844; AAK73125.1; -
DR EMBL; AK018632; BAB31317.1; -
DR MGD; MGI:191857; 9130017C17Rik.
DR InterPro; IPR001683; PX.
DR InterPro; IPR008941; TPR-like.
DR Pfam; PF00787; PX; 1.
DR SMART; SM00312; PX; 1.
DR PROSITE; PS0195; PX; 1.
DR TRANSPORT; Protein transport.
FT DOMAIN 75
SQ SEQUENCE 313 AA; 35998 MW; 88FCD04FA22707C3 CRC64;

Query Match
Best Local Similarity 76.0%; Score 1253.5; DB 1; Length 313;
Matches 244; Conservative 25; Mismatches 43; Indels 3; Gaps 1;

D5 1 MASPEHSGSCMGPICTQARTQOEAPATGPDLPHPGPDGHLTHSGSSNMTTREL 60
D5 1 MASPEHSGSGMGPIQCRTRTRQEVLPFGPDLPFCGPE---EAQDGSSNMTTREL 57
QY 61 QCYWQKQKRWKVKLLFETASARIEKSKVFVYQIIVTQTSFDNNKAVLERRYSDF 120
D5 58 QEHQKQKRWKVKLLFETASARIEKSKVFVYQIIVTQTSFDNNKAVLERRYSDF 117
QY 121 AKLQKALLKTFREIEDVEFPKHLTGNFAEMICERRALQEVLLGLLYALRCVRRSREF 180
D5 118 ERLOKALLKTFREIEDVEFPKHLTGNFAEMICERRALQEVLLGLLYALRCVRRSREF 177
QY 181 LDFLTPELBEAGCLRAGQYPRALQLLRLVLPQEKLTACHPAAVPAALCAVLLCHRD 240
D5 178 LDFLTPELBEAGCLRAGQYPRALQLLRLVLPQEKLTACHPAAVPAALCAVLLCHRD 237
QY 241 DRPAEFAAGERALQRLQAREGHRYVAPLLDAMVRLAYALGKDFVTLQELERLSQIRPT 300
D5 238 ERPAEFAAGERALQRLQAREGHRYVAPLLDAMVRLAYALGKDFVTLQELERLSQIRPT 297
QY 301 PRGTLKELTVREYL 315
D5 298 HRDATLKELTVREYL 312

RESULT 2
SNXL HUMAN
ID SNXL HUMAN STANDARD; PRT; 373 AA.
AC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sorting nexin 21.
GN SNX21 OR C20ORF161.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hong W.;
RT "A new member (SNX21) of the sorting nexin protein family.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Zeng W., Yuan W., Zhu Y., Jiao W., Wu X.;
RT "Cloning and characterizing a new member (SNX21) of the sorting nexin protein family.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Stavrides G.S., Huckle E.J., Deloukas P.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

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```

RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhali P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Letiaelaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie I.J., McLean K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.P., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- FUNCTION: May be involved in several stages of intracellular
CC trafficking (By similarity).
CC -!- SIMILARITY: Belongs to the sorting nexin family.
CC -!- SIMILARITY: Contains 1 phox homology (PX) domain.
CC
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CC
CC EMBL; AF395844; AAK73126.1; -
CC EMBL; AF523834; AAM77915.1; -
CC EMBL; AL591562; CAC39140.1; -
CC EMBL; AL008726; CAC36011.1; -
CC Genew; HSCN:16154; C20orf161.
CC InterPro; IPR001683; PX.
CC InterPro; IPR008941; TPR-like.
CC Pfam; PF00787; PX; 1.
CC SMART; SM00312; PX; 1.
CC PROSITE; PS0195; PX; 1.
CC TRANSPORT; Protein transport.
FT DOMAIN 129 246
FT CONFLICT 97 99 ERS -> GD (IN REF. 4).
SQ SEQUENCE 373 AA; 41365 MW; 83E4A752BAEA7B5 CRC64;

Query Match
Best Local Similarity 25.1%; Score 413.5; DB 1; Length 373;
Matches 108; Conservative 44; Mismatches 120; Indels 33; Gaps 6;

QY 31 GPD-LP-----HPGPDGHLDTHTSLSSNMTTRELQYQWQKRWKVKLL 77
D5 81 GPDQPLGDTSGEDAERSPPDGQW-----GQLARQLQDFWKSNTLAPQRL 132
QY 78 FEIASARIEKSKVFVYQIIVTQTSFDNNKAVLERRYSDFAKLQKALLTFREIED 137
D5 133 FEVTSANVVKDPSKVKVLYTLAVIGPGPDQCPAQISRRYSDFERLHRLNQPRGPM 192
QY 138 VEFPEKHLTGNFAEMICERRALQEVLLGLLYALRCVRRSREFLDTPELBEAGCL 197
D5 193 ISFPRKRLRNPTAETIARRSRAFEQFLGHLQAVPELHAPLODFVFLPELRRAQSL 252
QY 198 AGQYPRALQLLRLVLPQEKLTACHPAAVPAALCAVLLCHRDLPRAEFAAGERAL 256
D5 253 TGLFREALANANWLOQAQGLTSGPDRPLTLGLAVCHQELDPGEARACCEKAQL 312

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2004, 09:29:08 ; Search time 45 Seconds
(without alignments)
2215.639 Million cell updates/sec

Title: US-09-816-697A-2

Perfect score: 1650

Sequence: 1 MASPEHPSGPGMGPIQTCT.....RRTPRGITLKELTVREYLH 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	1650	100.0	316	4 Q7Z614	Q7Z614 homo sapien
2	1245.5	75.5	313	11 Q8CHQ3	Q8CHQ3 mus musculus
3	517	31.3	129	4 Q8IVS9	Q8IVS9 homo sapien
4	264	16.0	184	4 Q8WY78	Q8WY78 homo sapien
5	210	12.7	326	5 Q9VQ51	Q9VQ51 drosophila
6	174.5	10.6	199	4 Q8WUR6	Q8WUR6 homo sapien
7	122.5	7.4	398	13 Q7T332	Q7T332 brachydanio
8	122	7.4	152	4 Q14612	Q14612 homo sapien
9	122	7.4	337	11 Q91WE1	Q91WE1 mus musculus
10	117	7.1	952	10 Q9XIM1	Q9XIM1 arabidopsis
11	116	7.0	1010	3 Q9USN1	Q9USN1 schizosacch
12	115.5	7.0	450	5 Q95RK3	Q95RK3 drosophila
13	115.5	7.0	646	5 Q8MKN4	Q8MKN4 drosophila
14	115	7.0	248	16 Q8XSS5	Q8XSS5 ralatonia s
15	114.5	6.9	531	5 Q9W486	Q9W486 drosophila
16	113	6.8	169	11 Q9CRB0	Q9CRB0 mus musculus

17	111.5	6.8	1232	5 Q9UIQ7	Q9UIQ7 caenorhabdi
18	111	6.7	473	13 Q90990	Q90990 gallus gall
19	110.5	6.7	577	10 Q941X3	Q941X3 oryza sativ
20	110	6.7	336	11 Q8BMQ5	Q8BMQ5 mus musculu
21	109.5	6.6	581	11 Q8BX57	Q8BX57 mus musculu
22	109.5	6.6	582	11 Q91WB6	Q91WB6 mus musculu
23	108.5	6.6	652	16 Q828M0	Q828M0 streptomyce
24	107.5	6.5	519	11 Q80TZ1	Q80TZ1 mus musculu
25	107.5	6.5	526	11 Q8K4T6	Q8K4T6 rattus norv
26	107.5	6.5	532	11 Q7TQL6	Q7TQL6 mus musculu
27	107	6.5	441	16 Q88FT0	Q88FT0 pseudomonas
28	107	6.5	520	5 Q9VK31	Q9VK31 drosophila
29	106.5	6.5	539	11 Q8K4V4	Q8K4V4 rattus norv
30	106.5	6.5	579	11 Q7TNZ7	Q7TNZ7 rattus norv
31	104.5	6.3	1065	10 Q8H7X9	Q8H7X9 oryza sativ
32	104	6.3	545	5 Q861F6	Q861F6 dictyosteli
33	103.5	6.3	1006	10 Q8S018	Q8S018 oryza sativ
34	103.5	6.3	1096	10 Q7X7B5	Q7X7B5 mus musculu
35	102	6.2	1359	11 Q8K380	Q8K380 mus musculu
36	101.5	6.2	450	11 Q91YJ2	Q91YJ2 mus musculu
37	101	6.1	1325	4 Q9UG16	Q9UG16 homo sapien
38	101	6.1	2452	4 Q7Z6M5	Q7Z6M5 homo sapien
39	100.5	6.1	344	4 Q8N4U3	Q8N4U3 homo sapien
40	100.5	6.1	450	4 Q96CA3	Q96CA3 homo sapien
41	100.5	6.1	578	4 Q7Z7A4	Q7Z7A4 homo sapien
42	99.5	6.0	515	4 Q96R07	Q96R07 homo sapien
43	99.5	6.0	649	4 Q9NKB8	Q9NKB8 homo sapien
44	99.5	6.0	1065	10 Q91WZ8	Q91WZ8 oryza sativ
45	99	6.0	437	11 Q8CE50	Q8CE50 mus musculu

ALIGNMENTS

RESULT 1

Q7Z614 PRELIMINARY; PRT; 316 AA.
 AC Q7Z614
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Selectin ligand interactor cytoplasmic-1.
 GN SLIC1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shih H.H., Lorenz M., Sako D., Bridges K., Kriz R., Shaw G.D.;
 RT "SLIC-1: A Novel Sorting Nexin that Affects Subcellular Distribution of PSG1-1.";
 RT of PSG1-1.";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY302441; AAP58362.1; --
 KW Lectin; Selectin
 SQ SEQUENCE 316 AA; 36177 MW; 48D06CF4490907F4 CRC64;

Query Match 100.0%; Score 1650; DB 4; Length 316;
 Best Local Similarity 100.0%; Pred. No. 4.3e-132;
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASPEHPSGPGMGPIQTCTARTQOEAPATGPDLPHPGPDGHLDTHTSGLSNSSMTREL 60
 Db 1 MASPEHPSGPGMGPIQTCTARTQOEAPATGPDLPHPGPDGHLDTHTSGLSNSSMTREL 60
 Qy 61 QQYWNOKCWMKHVKLLFETASARIEBKSKFVYVYQIIVITQTSFNNKAVLERYSD 120
 Db 61 QQYWNOKCWMKHVKLLFETASARIEBKSKFVYVYQIIVITQTSFNNKAVLERYSD 120
 Qy 121 AKLQALKKTFREIEDEVFPKHLTGNFAEMICERRALQEVYLGILYATRCVRRSREF 180
 Db 121 AKLQALKKTFREIEDEVFPKHLTGNFAEMICERRALQEVYLGILYATRCVRRSREF 180

QY 181 LDFLTRPELREAFGCLRAGQYPRALLELVLPLOEKLTAKHCPAAAVPALCAVLLCHRD 240
Db 181 LDFLTRPELREAFGCLRAGQYPRALLELVLPLOEKLTAKHCPAAAVPALCAVLLCHRD 240
QY 241 DRPAFAAAGERALQRLQAREGHRYYPALLDAMVRLAYALGKDFVTLQERLEESQLRRPT 300
Db 241 DRPAFAAAGERALQRLQAREGHRYYPALLDAMVRLAYALGKDFVTLQERLEESQLRRPT 300
QY 301 PRGITLKELTVREYLH 316
Db 301 PRGITLKELTVREYLH 316
RESULT 2
Q8CHQ3
ID Q8CHQ3 PRELIMINARY; PRT; 313 AA.
AC Q8CHQ3
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DE 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RIKEN CDNA 9130017C17 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Lung;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC039809; AAH39809.1; -.
DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001683; PX.
DR InterPro; IPR008941; TPR-like.
DR Pfam; PF00787; PX; 1.
DR SMART; SM00312; PX; 1.
DR PROSITE; PS50195; PX; 1.
SQ SEQUENCE 313 AA; 36018 MW; F1236D0A2521C34 CRC64;

Query Match 75.5%; Score 1245.5; DB 11; Length 313;
Best Local Similarity 77.1%; Pred. No. 1e-97;
Matches 243; Conservative 25; Mismatches 44; Indels 3; Gaps 1;
QY 1 MASPEHSGPCMGPICTOCTARTQOAPATGPDLPHPGPGDGLDTHSGLSNSSMTTREL 60
Db 1 MASPEHSGPCMGPICTOCTARTQOAPATGPDLPHPGPGDGLDTHSGLSNSSMTTREL 60
QY 61 QQYQWQKCRWKHVLLFFETASARIEERKVKFVYQIIIVIQGSPDNKAVLERYSD 120
Db 58 QEHQWQKCRWKHVLLFFETASARIEERKVKFVYQIIIVIQGSPDNKAVLERYSD 117
QY 12- AKLOKALLTFREIEDVFPKRLTGNTAFBEMICERRALQYILGLLYAIRCVRERSREF 180
Db 118 ERLQALLKRFQPELVDVTPKRLTGNTAFBEMICERRALQYILGLLYAIRCVRERSREF 177
QY 181 LDFLTRPELREAFGCLRAGQYPRALLELVLPLOEKLTAKHCPAAAVPALCAVLLCHRD 240
Db 178 LDFLTRPELREAFGCLRAGQYPRALLELVLPLOEKLTAKHCPAAAVPALCAVLLCHRD 237
QY 241 DRPAFAAAGERALQRLQAREGHRYYPALLDAMVRLAYALGKDFVTLQERLEESQLRRPT 300
Db 238 ERPAFAAAGERALQRLQAREGHRYYPALLDAMVRLAYALGKDFVTLQERLEESQLRRPT 297
QY 301 PRGITLKELTVREYL 315
Db 298 HRDATLKEJTVREYL 312
RESULT 3
Q8IV59
ID Q8IV59 PRELIMINARY; PRT; 129 AA.
AC Q8IV59
DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
OS Similar to RIKEN CDNA 9130017C17 gene.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027944; AAH27944.1; -.
SQ SEQUENCE 129 AA; 14186 MW; 7037F3ABC0033C43 CRC64;
Query Match 31.3%; Score 517; DB 4; Length 129;
Best Local Similarity 98.9%; Pred. No. 3e-36;
Matches 94; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASPEHSGPCMGPICTOCTARTQOAPATGPDLPHPGPGDGLDTHSGLSNSSMTTREL 60
Db 1 MASPEHSGPCMGPICTOCTARTQOAPATGPDLPHPGPGDGLDTHSGLSNSSMTTREL 60
QY 61 QQYQWQKCRWKHVLLFFETASARIEERKVKFVY 95
Db 61 QQYQWQKCRWKHVLLFFETASARIEERKVKFVY 95

RESULT 4
Q8WY78
ID Q8WY78 PRELIMINARY; PRT; 184 AA.
AC Q8WY78
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DE 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE P3993 (Hypothetical protein FLJ34040) (Hypothetical protein FLJ38532).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Qin W.X.; Zhou X.M.; Zhang P.P.; Jiang H.Q.; Huang Y.; Wan D.F.;
GU J.R.;
RT "Novel human cDNA clones with function of inhibiting cancer cell growth."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Kawakami B.; Sugiyama A.; Takemoto M.; Sugiyama T.; Irie R.;
RA Osuki T.; Sato H.; Ota T.; Wakamatsu A.; Ishii S.; Yamamoto J.;
RA Isono Y.; Kawai-Hio Y.; Saito K.; Nishikawa T.; Kimura K.;
RA Yamashita H.; Matsumoto K.; Nakamura Y.; Sekine M.; Kikuchi H.; Kanda K.;
RA Wagatsuna M.; Murakawa K.; Kanehori K.; Takahashi-Fujii A.; Oshima A.;
RA Suzuki Y.; Sugano S.; Nagahara K.; Masuho Y.; Nagai K.; Isogai T.;
RT "NEDO human cDNA sequencing project."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258570; AG23773.1; -.
DR EMBL; AK091359; BAC03646.1; -.
DR EMBL; AK095851; BAC04637.1; -.
DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001683; PX.
DR InterPro; IPR008941; TPR-like.
DR PROSITE; PS50195; PX; 1.
KW Hypothetical protein.
SQ SEQUENCE 184 AA; 20612 MW; C3697FE2A1B19559 CRC64;
Query Match 16.0%; Score 264; DB 4; Length 184;
Best Local Similarity 37.3%; Pred. No. 1.5e-14;
Matches 69; Conservative 27; Mismatches 77; Indels 12; Gaps 3;

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OM protein - protein search, using sw model

Run on: June 7, 2004, 09:29:07 ; Search time 59 Seconds

(without alignments)

1513.305 Million cell updates/sec

Title:

US-09-816-697A-2

Perfect score: 1650

Sequence: 1 MASPEHPGSGCGMPITQCT.....RRTPRGITLXELTVREYLH 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A. Genesep 23Jan04:*

1: Genesep1980s:*

2: Genesep1990s:*

3: Genesep2000s:*

4: Genesep2001s:*

5: Genesep2002s:*

6: Genesep2003as:*

7: Genesep2003bs:*

8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1650	100.0	316	4	AAG79225 Amino aci
2	1650	100.0	316	6	AAO26235 MDDT rela
3	1650	100.0	316	6	ABO07143 Novel hum
4	1650	100.0	334	4	AAG79120 Amino aci
5	1640	99.4	316	7	ADC31008 Human nov
6	464	28.1	148	3	AAH43067 Human ORF
7	333	20.2	239	6	ABU11470 Human MDD
8	324	19.6	156	4	AAH89008 Human imm
9	264	16.0	184	5	AAO17131 Human can
10	264	16.0	184	7	ADB64274 Human pro
11	255	15.5	580	4	ABG27894 Novel hum
12	249	15.1	93	4	AAH84390 Human imm
13	185.5	11.2	295	4	ABH59625 Drosophil
14	125.5	7.6	212	4	ABG23125 Novel hum
15	118	7.2	173	4	AAU17487 Novel sig
16	118	7.2	173	7	ADB94195 Human nov
17	114.5	6.9	431	4	ABH59662 Drosophil
18	112.5	6.8	168	3	ABH45187 Human sec
19	112.5	6.8	541	5	ABH08158 Human cyt
20	108.5	6.6	141	4	AAU17481 Novel sig
21	108.5	6.6	141	7	ADB94189 Human nov
22	107.5	6.5	166	4	ABG22895 Novel hum
23	107	6.5	441	6	ABU39601 Protein e
24	107	6.5	520	4	ABH61499 Drosophil
25	103.5	6.3	245	4	ABG20248 Novel hum

26	103.5	6.3	320	4	ABG07654	Abg07654 Novel hum
27	102	6.2	2472	7	ADE55351	Ad55351 Rat Prote
28	100.5	6.1	344	5	AAE23382	Aae23382 Human int
29	100.5	6.1	577	4	AAE02775	Aae02775 Human PRO
30	100.5	6.1	578	5	ABB97328	Abb97328 Novel hum
31	99.5	6.0	156	4	ABG22890	Abg22890 Novel hum
32	99.5	6.0	649	4	AAH56680	Aah56680 Novel pro
33	99.5	6.0	705	4	AAH39328	Aah39328 Human pol
34	99.5	6.0	714	4	AAH41114	Aah41114 Human pol
35	99	6.0	141	4	AAU17470	Aau17470 Novel sig
36	99	6.0	141	7	ADB94178	Adb94178 Human nov
37	99	6.0	2472	7	ADE55353	Ad55353 Human PRO
38	99	6.0	2477	7	ABR84742	AbR84742 Human spe
39	98.5	6.0	66	4	AAU17617	Aau17617 Novel sig
40	98.5	6.0	66	7	ADB94325	AdB94325 Human nov
41	98.5	6.0	165	4	AAU17438	Aau17438 Novel sig
42	98.5	6.0	165	7	ADB94146	AdB94146 Human nov
43	98	5.9	278	4	AAU17486	Aau17486 Novel sig
44	98	5.9	278	7	ADB94194	AdB94194 Human nov
45	98	5.9	585	4	ABB62665	Abb62665 Drosophil

ALIGNMENTS

RESULT 1

AAG79225

ID AAG79225 standard; protein; 316 AA.

XX AC AAG79225;

XX XX

DT 03-JAN-2002 (first entry)

XX XX

DE Amino acid sequence of a human PSGL-1 binding protein.

XX XX

KW Human; P-selectin glycoprotein ligand binding protein;

KW PSGL-1 binding protein; selectin ligand interactor cytoplasmic-1 protein;

KW SLIC-1 protein; signal transduction; cytoskeletal organization;

KW immune response; inflammatory response; cell adhesion; cell migration;

KW cell activation; cell growth; cell differentiation; cell proliferation;

KW immune system disorder; cardiovascular disorder; haematopoietic disorder;

KW thrombotic disorder.

XX OS Homo sapiens.

XX XX

PN WO200173028-A2.

XX XX

PD 04-OCT-2001.

XX XX

PF 23-MAR-2001; 2001WO-US009469.

XX XX

PR 24-MAR-2000; 2000US-0192104P.

XX XX

PA (GEMY) GENETICS INST INC.

XX XX

PI Lorenz M, Kriz R, Weich N, Shaw GD;

XX XX

DR WPI; 2001-616502/71.

XX XX

DR N-PSDB; AA165832.

XX XX

PT Isolated polynucleotides (SLIC-1) which encode novel P-selectin

PT glycoprotein ligand (PSGL-1) binding protein, useful as targets for

PT developing modulating agents to regulate a variety of cellular processes

PT including signal transduction.

XX Claim 14; Fig 1; 108pp; English.

PS The present sequence represents a human P-selectin glycoprotein ligand

PS (PSGL-1) binding protein. The protein is a member of the selectin ligand

PS interactor cytoplasmic (SLIC-1) family. The SLIC-1 polynucleotides and

CC polypeptides are useful as targets for developing modulating agents to

CC regulate a variety of cellular processes such as signal transduction, and

CC cytoskeletal organization, immune and inflammatory responses, inter- and

CC intra-cellular communication, adhesion, migration, cell activation,
 CC growth, differentiation and proliferation. The SLIC-1 proteins provide
 CC novel diagnostic targets and therapeutic agents to control or modulate
 CC SLIC-1 molecule-associated disorders such as an inflammatory or immune
 CC system disorder, a cardiovascular disorder, a cellular proliferation,
 CC activation, adhesion, growth, differentiation or migration disorder or a
 CC haematopoietic or thrombotic disorder
 XX
 SQ Sequence 316 AA;

Query Match 100.0%; Score 1650; DB 4; Length 316;
 Best Local Similarity 100.0%; Pred. No. 5.7e-163;
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASPEHPSGCMGPITQCTARTQEQAPATGPDLPHPGDPGHLOTHSGLSNSTMREL 60
 DB 1 MASPEHPSGCMGPITQCTARTQEQAPATGPDLPHPGDPGHLOTHSGLSNSTMREL 60

QY 61 QQYWNQKCRWKHKVLLFEIASARIEERKVKSVVYQIIVITQSGFNNKAVLERYSDP 120
 DB 61 QQYWNQKCRWKHKVLLFEIASARIEERKVKSVVYQIIVITQSGFNNKAVLERYSDP 120

QY 121 AKIQALLKTFREIEDVEFPKRLTGNFABEMICERRALQEQYLGLLYAIRCVRRESREF 180
 DB 121 AKIQALLKTFREIEDVEFPKRLTGNFABEMICERRALQEQYLGLLYAIRCVRRESREF 180

QY 181 LDFLTRPELRAFCLRAGQYPRALELLRLVLPLOEKLTAHCPCAAAVPALCAVLLCHRD 240
 DB 181 LDFLTRPELRAFCLRAGQYPRALELLRLVLPLOEKLTAHCPCAAAVPALCAVLLCHRD 240

QY 241 DRPAEAPAGERALQRLQAREGHRYAPLDDAMVRLAYALGKQFVTLQERLESQLRPT 300
 DB 241 DRPAEAPAGERALQRLQAREGHRYAPLDDAMVRLAYALGKQFVTLQERLESQLRPT 300

QY 301 PRGITLKELTVREYLH 316
 DB 301 PRGITLKELTVREYLH 316

RESULT 2

AAO26235 ID AAO26235 standard; protein; 316 AA.

AC AAO26235;

DC 10-APR-2003 (first entry)

DE MDDT related human protein SEQ ID No 13.

KW Cytostatic; antiatherosclerotic; osteopathic; antiarteriosclerotic;
 KW hepatotropic; antipsoriatic; antiallergic; antianemic; antiasthmatic;
 KW antithyroid; antiinflammatory; antihelminthic; antidiabetic; nephrotropic;
 KW ophthalmological; immunosuppressive; dermatological; antiulcer;
 KW antirheumatic; antiarthritic; antibacterial; virucide; fungicide;
 KW antiparasitic; protozoacide; tranquiliser; vulnerary; anti-HIV;
 KW neurotropic; neuroprotective; anticonvulsant; cerebroprotective;
 KW neuroleptic; molecules for disease detection and treatment; MDDT;
 KW immunogen; cancer; actinic keratosis; arteriosclerosis; atherosclerosis;
 KW bursitis; cirrhosis; hepatitis; psoriasis; AIDS; rheumatoid arthritis;
 KW adult respiratory distress syndrome; Addison's disease; allergy; anaemia;
 KW asthma; osteoporosis; autoimmune; haemolytic anaemia; scleroderma;
 KW autoimmune thyroiditis; Crohn's disease; atopic dermatitis;
 KW diabetes mellitus; Graves' disease; glomerulonephritis;
 KW systemic lupus erythematosus; systemic sclerosis; ulcerative colitis;
 KW haemodialysis; uveitis; trauma; Alzheimer's; Pick disease;
 KW Parkinson disease; amyotrophic lateral sclerosis; epilepsy; stroke;
 KW Huntington's disease; multiple sclerosis; dementia;
 KW extrapyramidal disorder; motor neuron disorder; central nervous system;
 KW neuromuscular disorder; metabolic; endocrine; toxic myopathy;
 KW periodic paralysis; mental disorder; human.

XX Homo sapiens.

PN WO200296951-A1.

XX 05-DEC-2002.

PF 24-MAY-2002; 2002WO-US016676.

XX 25-MAY-2001; 2001US-0293723P.

PR 01-JUN-2001; 2001US-0295257P.

PR 08-JUN-2001; 2001US-0297220P.

PR 21-JUN-2001; 2001US-0300526P.

PR 29-JUN-2001; 2001US-0301874P.

PR 22-FEB-2002; 2002US-0359413P.

XX (INCY-) INCYTE GENOMICS INC.

XX Tang TY, Yue H, Baughn MR, Duggan BM, Warren BA, Bandman O;
 Richardson TW, Burford N, Sanjanwala B, Becha SD, Yao MG, Yang J;
 Tran UK, Hafalia AJA, Griffin JA, Swarnakar A, Elliott VS;
 Recipon SA, Khan FA, Lee EA, Yue H, Lu DAM, Wallia NK, Thangavelu K;
 Arvizu CS, Xu Y, Ison CH, Huang J, Ding L, Honchell CD;
 Borowsky ML, Emerling BM, Peterson DP, Lu Y, Ramkumar J, Mason PM;
 Zebariadian Y, Azimzai Y, Stuve LL, Kamigaki LL, Barroso I, Lee S;
 Kable AE;

XX WPI; 2003-140448/13.

DR N-PSDB; AAK99588.

XX Novel molecules for disease detection and treatment and polynucleotide
 encoding them useful for diagnosing, preventing or treating cell
 PT proliferative, autoimmune/inflammatory, neurological and developmental
 PT disorders.

XX Claim 68; Page 188-189; 260pp; English.

XX The invention relates to an isolated polypeptide chosen from molecules
 CC for disease detection and treatment (MDDT), comprising a one of 39 114-
 CC 1250 residue amino acid sequences, given in the specification, or a
 CC biologically active or immunogenic fragment of the isolated polypeptide.
 CC The isolated polypeptide is useful for screening a compound for
 CC effectiveness as an agonist or antagonist of the isolated polypeptide.
 CC The isolated polypeptide is also useful as an immunogen for preparing
 CC polyclonal or monoclonal antibodies by hybridoma technology. The isolated
 CC polypeptide and its encoding polynucleotide are useful for diagnosis,
 CC treatment and prevention of cancer, actinic keratosis, arteriosclerosis,
 CC atherosclerosis, bursitis, cirrhosis, hepatitis, psoriasis, AIDS, adult
 CC respiratory distress syndrome, Addison's disease, allergies, anaemia,
 CC asthma, atherosclerosis, osteoporosis, autoimmune haemolytic anaemia,
 CC autoimmune thyroiditis, Crohn's disease, atopic dermatitis, diabetes
 CC mellitus, Graves' disease, glomerulonephritis, rheumatoid arthritis,
 CC scleroderma, systemic lupus erythematosus, systemic sclerosis, ulcerative
 CC colitis, haemodialysis, uveitis, viral, bacterial, fungal, parasitic,
 CC protozoal, helminthic infections, trauma, Alzheimer's and Pick disease,
 CC Parkinson disease, amyotrophic lateral sclerosis, epilepsy, stroke,
 CC Huntington's disease, multiple sclerosis, dementia, and other
 CC extrapyramidal disorder, motor neuron disorder, and other developmental
 CC disorders of the central nervous system, neuromuscular disorders,
 CC metabolic, endocrine and toxic myopathies, periodic paralysis, mental
 CC disorders including mood, anxiety and schizophrenic disorders, anaemia,
 CC renal tubular acidosis, epilepsy, hypothyroidism, glaucoma, sensorineural
 CC hearing loss and cataract. This sequence represents a human MDDT protein
 CC relating to the invention

XX Sequence 316 AA;

Query Match 100.0%; Score 1650; DB 6; Length 316;

Best Local Similarity 100.0%; Pred. No. 5.7e-163;

Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASPEHPSGCMGPITQCTARTQEQAPATGPDLPHPGDPGHLOTHSGLSNSTMREL 60

DB 1 MASPEHPSGCMGPITQCTARTQEQAPATGPDLPHPGDPGHLOTHSGLSNSTMREL 60

QY 61 QQYWNQKCRWKHKVLLFEIASARIEERKVKSVVYQIIVITQSGFNNKAVLERYSDP 120

GenCore version 5.1.6
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OX protein - protein search, using sw model

Run on: June 7, 2004, 09:31:58 ; Search time 48 Seconds
(without alignments)
1852.146 Million cell updates/sec

Title: US-09-816-697A-2
Perfect score: 1650
Sequence: 1 MASPEHPSGCMGPITQCT.....RR2PRGTLKELTVREYLH 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1650	100.0	316	9	US-09-816-697-2
2	1650	100.0	316	15	US-10-161-927-2
3	1650	100.0	334	14	US-10-240-046A-5
4	1134	68.7	222	14	US-10-029-386-32848
5	264	16.0	184	15	US-10-104-047-2428
6	264	16.0	184	15	US-10-108-260A-3381
7	118	7.2	173	9	US-09-764-868-1052
8	112.5	6.8	344	12	US-10-112-944-322
9	112.5	6.8	541	12	US-10-415-187-2
10	108.5	6.6	141	9	US-09-764-868-1046
11	108.5	6.6	652	14	US-10-156-761-14177
12	107	6.5	441	12	US-10-282-122A-67525
13	103.5	6.3	387	16	US-10-408-765A-1906
14	102.5	6.2	443	15	US-10-369-493-1843
15	101.5	6.2	732	12	US-10-425-114-56615

16	100.5	6.1	344	16	US-10-399-455-9	Sequence 9, Appli
17	99.5	6.0	515	16	US-10-408-765A-2323	Sequence 2323, Ap
18	99.5	6.0	696	14	US-10-122-805-4	Sequence 4, Appli
19	99	6.0	1471	9	US-09-764-868-1035	Sequence 1035, Ap
20	99	6.0	2477	14	US-10-360-053-28	Sequence 28, Appl
21	99	6.0	2477	16	US-10-408-765A-238	Sequence 238, App
22	98.5	6.0	66	9	US-09-764-868-1182	Sequence 1182, Ap
23	98.5	6.0	165	9	US-09-764-868-1003	Sequence 1003, Ap
24	98	5.9	278	9	US-09-764-868-1051	Sequence 1051, Ap
25	97	5.9	270	15	US-10-168-659-6	Sequence 6, Appli
26	97	5.9	395	15	US-10-080-334-246	Sequence 246, App
27	97	5.9	595	15	US-10-080-334-247	Sequence 247, App
28	96.5	5.8	447	14	US-10-106-638-4948	Sequence 4948, Ap
29	96.5	5.8	455	12	US-10-276-774-1983	Sequence 1983, Ap
30	96	5.8	441	12	US-10-282-122A-66398	Sequence 66398, A
31	96	5.8	595	12	US-10-170-385-319	Sequence 319, App
32	95.5	5.8	259	14	US-10-233-131-18	Sequence 18, Appl
33	95.5	5.8	259	15	US-10-240-145-70	Sequence 70, Appl
34	95.5	5.8	576	15	US-10-369-493-22712	Sequence 22712, A
35	95.5	5.8	1911	12	US-10-220-955-24	Sequence 24, Appl
36	95.5	5.8	2392	16	US-10-408-765A-1880	Sequence 1880, Ap
37	95.5	5.8	2930	10	US-09-957-837A-2	Sequence 2, Appli
38	95.5	5.8	3031	15	US-10-165-216-6	Sequence 6, Appli
39	95.5	5.8	3521	15	US-10-165-216-2	Sequence 2, Appli
40	95.5	5.8	3529	15	US-10-165-216-8	Sequence 8, Appli
41	95.5	5.8	3657	15	US-10-165-216-10	Sequence 10, Appl
42	95	5.8	608	14	US-10-204-887-87	Sequence 87, Appl
43	95	5.8	943	12	US-10-282-122A-76714	Sequence 76714, A
44	94.5	5.7	1049	12	US-10-168-582-7	Sequence 7, Appli
45	94.5	5.7	1049	14	US-10-317-835-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-09-816-697-2

; Sequence 2, Application US/09816697

; Patent No. US20020037840A1

; GENERAL INFORMATION:

; APPLICANT: Lorenz, M., et al.

; TITLE OF INVENTION: A NOVEL P-SELECTIN GLYCOPROTEIN LIGAND (PSGL-1)

; FILE REFERENCE: GFN-5380

; CURRENT APPLICATION NUMBER: US/09/816,697

; PRIOR FILING DATE: 2001-03-23

; PRIOR FILING DATE: 60/192,104

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-816-697-2

Query Match 100.0%; Score 1650; DB 9; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.2e-151;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MASPEHPSGCMGPITQCTARTQOAPATGPDPHPGPGHLDTHSGLSNSMTTREL	60
Db	1	MASPEHPSGCMGPITQCTARTQOAPATGPDPHPGPGHLDTHSGLSNSMTTREL	60
Qy	61	QQWQKQKRWKLVLLFEIASARIERKYSKFWVYQIIVIQGSPNNKAVLERRYSDF	120
Db	61	QQWQKQKRWKLVLLFEIASARIERKYSKFWVYQIIVIQGSPNNKAVLERRYSDF	120
Qy	121	AKLQKALLTFREIEDEVEFPKHLTGNGFAEMICERRALQYGLLYAIRCVRRSREF	180
Db	121	AKLQKALLTFREIEDEVEFPKHLTGNGFAEMICERRALQYGLLYAIRCVRRSREF	180
Qy	181	LOFLTEPELRERAGCLRAGQYPRALELLRLVLPQKLTACCPAAVPAALCAVLLCHRD	240

Db 181 LDFTLRPELREAFGCLRAGQYPRALELLRLVLPQEKLTARCPAAAVPALCAVLLCHRD 240
QY 241 DRPAEFAAAGERALQRLQAREGHRYYPALDAMVRLAYALGKDFVTLQERLEESQLRRPT 300
Db 241 DRPAEFAAAGERALQRLQAREGHRYYPALDAMVRLAYALGKDFVTLQERLEESQLRRPT 300
QY 301 PRGITLKELTVREYJH 316
Db 301 PRGITLKELTVREYJH 316

RESULT 2

US-10-161-927-64

; Sequence 64, Application US/10161927

; Publication No. US20030235821A1

; GENERAL INFORMATION:

; APPLICANT: Zerhusen, Bryan D.

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Shenoy, Suresh G.

; APPLICANT: Miller, Charles E.

; APPLICANT: Hjal, Tord

; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Baumgartner, Jason C.

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gangolli, Esha A.

; APPLICANT: Vernet, Corine

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Li, Li

; APPLICANT: Pena, Carol E.A.

; APPLICANT: Gorman, Linda

; APPLICANT: Anderson, David W.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Patturajan, Meera

; APPLICANT: Stone, David J.

; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS

; FILE REFERENCE: THE SAME

; CURRENT APPLICATION NUMBER: US/10161927

; CURRENT FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: 60/295,661

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/295,607

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/296,404

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 60/296,418

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 60/296,575

; PRIOR FILING DATE: 2001-06-07

; PRIOR APPLICATION NUMBER: 60/297,414

; PRIOR FILING DATE: 2001-06-11

; PRIOR APPLICATION NUMBER: 60/297,567

; PRIOR FILING DATE: 2001-06-12

; PRIOR APPLICATION NUMBER: 60/298,528

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/325,685

; PRIOR FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: 60/299,133

; PRIOR FILING DATE: 2001-06-18

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 190

; SEQ ID NO 64

; LENGTH: 3-6

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-161-927-64

Query Match 100.0%; Score 1650; DB 15; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.2e-151;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASPEHPGSPGCMGPITQCTARTQOEAPATGPDLPHPGPDGHLDTSGLSNSSMTTREL 60
Db 1 MASPEHPGSPGCMGPITQCTARTQOEAPATGPDLPHPGPDGHLDTSGLSNSSMTTREL 60
QY 61 QOYWONOKCRWKHVKLLFEIASARIEERKVSFVYQIIVITQTSFDDNNKAVLERYSD 120
Db 61 QOYWONOKCRWKHVKLLFEIASARIEERKVSFVYQIIVITQTSFDDNNKAVLERYSD 120
QY 121 AKLOKALLKTFREIEDEVFPKHLTGNFAEMICERRALQEYLGLLYAIRCVRRSREF 180
Db 121 AKLOKALLKTFREIEDEVFPKHLTGNFAEMICERRALQEYLGLLYAIRCVRRSREF 180
QY 181 LDFTLRPELREAFGCLRAGQYPRALELLRLVLPQEKLTARCPAAAVPALCAVLLCHRD 240
Db 181 LDFTLRPELREAFGCLRAGQYPRALELLRLVLPQEKLTARCPAAAVPALCAVLLCHRD 240
QY 241 DRPAEFAAAGERALQRLQAREGHRYYPALDAMVRLAYALGKDFVTLQERLEESQLRRPT 300
Db 241 DRPAEFAAAGERALQRLQAREGHRYYPALDAMVRLAYALGKDFVTLQERLEESQLRRPT 300
QY 301 PRGITLKELTVREYJH 316
Db 301 PRGITLKELTVREYJH 316

RESULT 3

US-10-240-046A-5

; Sequence 5, Application US/10240046A

; Publication No. US20030190639A1

; GENERAL INFORMATION:

; APPLICANT: HUGOT, JEAN-PIERRE

; APPLICANT: THOMAS, GILLES

; APPLICANT: ZOUALI, MOHAMED

; APPLICANT: LESAGE, SUZANNE

; APPLICANT: CHAMAILLARD, MATHIAS

; TITLE OF INVENTION: GENES INVOLVED IN INTESTINAL INFLAMMATORY DISEASES AND USE

; FILE REFERENCE: THEREOF

; CURRENT APPLICATION NUMBER: US/10240046A

; CURRENT FILING DATE: 2003-04-02

; PRIOR APPLICATION NUMBER: PCT/FR 01/00935

; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: FR 00/03832

; PRIOR FILING DATE: 2000-03-27

; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 334

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-240-046A-5

Query Match 100.0%; Score 1650; DB 14; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.3e-151;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASPEHPGSPGCMGPITQCTARTQOEAPATGPDLPHPGPDGHLDTSGLSNSSMTTREL 60
Db 19 MASPEHPGSPGCMGPITQCTARTQOEAPATGPDLPHPGPDGHLDTSGLSNSSMTTREL 78
QY 61 QOYWONOKCRWKHVKLLFEIASARIEERKVSFVYQIIVITQTSFDDNNKAVLERYSD 120
Db 79 QOYWONOKCRWKHVKLLFEIASARIEERKVSFVYQIIVITQTSFDDNNKAVLERYSD 138
QY 121 AKLOKALLKTFREIEDEVFPKHLTGNFAEMICERRALQEYLGLLYAIRCVRRSREF 180
Db 139 AKLOKALLKTFREIEDEVFPKHLTGNFAEMICERRALQEYLGLLYAIRCVRRSREF 198
QY 181 LDFTLRPELREAFGCLRAGQYPRALELLRLVLPQEKLTARCPAAAVPALCAVLLCHRD 240
Db 199 LDFTLRPELREAFGCLRAGQYPRALELLRLVLPQEKLTARCPAAAVPALCAVLLCHRD 258
QY 241 DRPAEFAAAGERALQRLQAREGHRYYPALDAMVRLAYALGKDFVTLQERLEESQLRRPT 300

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OM protein - protein search, using sw model

Run on: June 7, 2004, 09:29:08 ; Search time 22 Seconds
(without alignments)
741.537 Million cell updates/sec

Title: US-09-816-697A-2

Perfect score: 1650

Sequence: 1 MASPEHPGSGCMGPITQCT.....RRPTRGITLKELTVREYLH 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 3

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	6.4	713	US-09-252-991A-32624	Sequence 32624, A
2	99.5	6.0	696	US-08-906-865-4	Sequence 4, Appl
3	99.5	6.0	696	US-09-129-668-4	Sequence 4, Appl
4	96	5.8	444	US-09-252-991A-31066	Sequence 31066, A
5	95.5	5.8	259	US-09-808-701A-18	Sequence 18, Appl
6	95.5	5.8	2930	US-09-417-822-2	Sequence 4397, Ap
7	94.5	5.7	393	US-09-107-532A-4397	Sequence 2, Appl
8	90	5.5	3072	US-09-413-814-93	Sequence 93, Appl
9	90	5.5	3079	US-09-413-814-80	Sequence 80, Appl
10	89	5.4	663	US-09-252-991A-30342	Sequence 30342, A
11	89	5.4	833	US-09-489-039A-9336	Sequence 9336, Ap
12	89	5.4	1201	US-09-252-991A-32259	Sequence 32259, A
13	88.5	5.4	430	US-09-489-039A-7580	Sequence 7580, Ap
14	88.5	5.4	533	US-09-252-991A-20347	Sequence 20347, A
15	87.5	5.3	340	US-09-134-000C-6526	Sequence 6526, Ap
16	87	5.3	391	US-09-489-039A-12724	Sequence 12724, A
17	87	5.3	674	US-09-134-000C-4004	Sequence 4004, Ap
18	85.5	5.2	522	US-08-625-322-2	Sequence 2, Appl
19	85	5.2	338	US-08-890-719-12	Sequence 12, Appl
20	85	5.2	523	US-09-252-991A-33001	Sequence 33001, A
21	84	5.1	486	US-08-821-355A-8	Sequence 8, Appl
22	84	5.1	486	US-09-003-687A-8	Sequence 8, Appl
23	84	5.1	486	US-09-136-605-8	Sequence 8, Appl
24	83	5.0	947	US-09-543-681A-6556	Sequence 6556, Ap
25	83	5.0	1326	US-09-688-188B-15	Sequence 15, Appl
26	83	5.0	1326	US-09-291-417D-15	Sequence 15, Appl
27	82.5	5.0	302	US-09-252-991A-21992	Sequence 21992, A

RESULT 1

US-09-252-991A-32624

Sequence 32624, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 32624

LENGTH: 713

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-32624

Query Match 6.4%; Score 106; DB 4; Length 713;

Best Local Similarity 24.0%; Pred. No. 0.0092;

Matches 102; Conservative 41; Mismatches 32; Indels 150; Gaps 26;

QY 4 PEHPG---SPGCMGPITQ-----CTATQOEAPATGPDLPHPGPDGHLD---44

Db 18 PEPPGGIVASEGC-GSISMLEFGKVLSSLCRPLGQESG-----LFHSSCSGHDDEPAS 70

QY 45 -----TH-SGLSS--NSSMTTREIQYQWQKCRKWHVKL-----76

Db 71 RVKKEAQPRSEVRHLSGASSPRSLFSSGAVYPMENQS---PHLSRVPTTQCNLS 127

QY 77 -----LFEIASARIEERKVKFVVQIIVQTGSPDNKAVLERRYSDFAKLQ 124

Db 128 FCDATPKDQIKYWLALHPKANLGE---TARQLYQ-----GLIELNQLVPE---ARLQ 174

QY 125 KALLKTFEEIEDVFPRKHLTCNFAEMIC-ERRR-----ALOEVLGLLYAIRC- 174

Db 175 ---LLSLFRPE---VHFVCAHLRHFNLQAIULDERPKIANLCQALQNLHAIQYKLVVQ 229

QY 175 ---RESREFLDFT---RPELEAFG-CLRAGQ-----YPRALELLLRV 211

Db 230 EAPRNSRDRQAQLLVGICQAIIRSLCGPLIRASQLYCPVEGLWLEHLQYQLASQSGVHR 289

QY 212 LPLOEKLTAHCP-----AAAVPALCNVLLCHR-----DLDRPAEFAAAGALQRLQAR- 260

Db 290 LAVRDELAKHTPGLSVEQAQYLLPLLLGGCARGCQNRNNIARLAEVLEPNSQLLSIQSATL 349

ALIGNMENTS

QY 261 ECHRYA-PILDMVR-----LAYALGKDF-----VTQRR-EESQIRPTP 301
DB 350 PGSLFIAVPOIDGPPRYSLYPETQLANALGIDTQPLVELIREYLLQPEARAKARLEPLI 409
QY 302 RGITL 306
DB 410 EGVTL 424

RESULT 2

US-08-906-865-4
; Sequence 4, Application US/08906865
; Patent No. 6040168
; GENERAL INFORMATION:
; APPLICANT: Greengard, Paul
; APPLICANT: Porton, Barbara
; APPLICANT: Kao, Hung-Teh
; TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,865
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 696 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: /desc = "Synapsin Ia"
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

US-08-906-865-4

Query Match 6.0%; Score 99.5; DB 3; Length 696;
Best Local Similarity 25.0%; Pred. No. 0.048;
Matches 72; Conservative 29; Mismatches 96; Indels 91; Gaps 17;

QY 4 PEHFG--SPGCM-GPITQCTARTQOEAPATGPDLPHPGPDGHLDTGSLSSNMTTREL 60
DB 32 PPPGAHSPGATPGGTATERSGVAPASPAAPSGSGGGGFFSSLSNAVKQT--- 88
QY 61 QQYWNQKCRWKHVKLLFEIASARIEERKVKFVVYQIIVITQGSFNNKA-----V 112
DB 89 -----AAAAATFSEQ-----VGGSGGAGRGGAASRVLLV 118
QY 113 LERRYSDFAKLQKALLKTFREEI-----EDVEFPR-----KHLTGNFAEMICERRALQY 164
DB 119 IDEPHTWAKYFKG--KKIHGEIDIKVEQAEFSDNLVAHANGGFSVDMVELRN----- 170

QY 165 LGLLYAIRCVRRSREFLDF-LTRPELREAFGCLRAGQYPRALELLRLVLPQEKLTARCP 223
DB 171 -----GVKVVRSUKP--DFVLIR---QHAFSMARNGDY-RSL-----VIGLQ----- 206
QY 224 AAAYPALCAVLLCHRDLDPRAPAAAGERALORLOAREGHRYVAPLLD 271
DB 207 YAGIPSVNLSHVSYNFCDKP-WVFAQVRLHKKLGTE-----FPLID 248

RESULT 3

US-09-129-668-4
; Sequence 4, Application US/09129668B
; Patent No. 6429010
; GENERAL INFORMATION:
; APPLICANT: Greengard, Paul
; APPLICANT: Porton, Barbara
; APPLICANT: Kao, Hung-Teh
; TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 600-1-202 CIP
; CURRENT APPLICATION NUMBER: US/09/129,668B
; CURRENT FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 08/906,865
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 4
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-129-668-4

Query Match 6.0%; Score 99.5; DB 4; Length 696;
Best Local Similarity 25.0%; Pred. No. 0.048;
Matches 72; Conservative 29; Mismatches 96; Indels 91; Gaps 17;

QY 4 PEHFG--SPGCM-GPITQCTARTQOEAPATGPDLPHPGPDGHLDTGSLSSNMTTREL 60
DB 32 PPPGAHSPGATPGGTATERSGVAPASPAAPSGSGGGGFFSSLSNAVKQT--- 88
QY 61 QQYWNQKCRWKHVKLLFEIASARIEERKVKFVVYQIIVITQGSFNNKA-----V 112
DB 89 -----AAAAATFSEQ-----VGGSGGAGRGGAASRVLLV 118
QY 113 LERRYSDFAKLQKALLKTFREEI-----EDVEFPR-----KHLTGNFAEMICERRALQY 164
DB 119 IDEPHTWAKYFKG--KKIHGEIDIKVEQAEFSDNLVAHANGGFSVDMVELRN----- 170
QY 165 LGLLYAIRCVRRSREFLDF-LTRPELREAFGCLRAGQYPRALELLRLVLPQEKLTARCP 223
DB 171 -----GVKVVRSUKP--DFVLIR---QHAFSMARNGDY-RSL-----VIGLQ----- 206
QY 224 AAAYPALCAVLLCHRDLDPRAPAAAGERALORLOAREGHRYVAPLLD 271
DB 207 YAGIPSVNLSHVSYNFCDKP-WVFAQVRLHKKLGTE-----FPLID 248

RESULT 4

US-09-252-991A-31066
; Sequence 31066, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142